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Genome Announcement

Genome sequence of *Xanthomonas sacchari* R1, a biocontrol bacterium isolated from the rice seed

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ABSTRACT

Xanthomonas sacchari, was first identified as a pathogenic bacterium isolated from diseased sugarcane in Guadeloupe. In this study, R1 was first isolated from rice seed samples from Philippines in 2002. The antagonistic ability against several rice pathogens raises our attention. The genomic feature of this strain was described in this paper. The total genome size of *X. sacchari* R1 is 5,000,479 bp with 4315 coding sequences (CDS), 59 tRNAs, 2rRNAs and one plasmid.

Xanthomonas comprise 27 species of plant-associated Gram-negative bacteria, which can infect important economical plants (Studholme et al., 2011). Although many of these species are plant-pathogen related, some strains have showed their potential application in industry such as xanthan gum production (Rosalam and England, 2006). In 2002, the previous members in our lab isolated R1 from rice seed samples from Philippines (Xie et al., 2003). This strain showed its antagonistic ability against *Burkholderia glumae*, which is a serious rice bacterial disease in the world (Ham et al., 2011).

Until now, only two *Xanthomonas sacchari* strains (LMG 476 and NCPPB 4393) were partial sequenced (NCBI data). Interestingly, both strains were isolated from diseased plants while no biocontrol strain has been sequenced until now. Here we present a summary classification and a set of features for *X. sacchari* R1 together with the description of the complete genomic sequencing and annotation.

The culture of strain R1 used to prepare genomic DNA for sequencing was a laboratory stock and grown on NB (Nutrient Broth, BD, USA) at 28 °C with vigorous shaking. 2 ml of culture broth was used to isolate DNA. Full genomic DNA was isolated by using Wizard Genomic DNA Purification Kit (Promega, Madison, WI, USA). The genome of R1 strain was done by Guhe info by using the PacBio RS II platform. Around 450Mb data was obtained with 60× average coverage. After quality control, genome assembly was done by SMRT Analysis 2.2.1 and the protein coding genes, tRNA and rRNA annotations was done by NCBI Prokaryotic Genome Annotation Pipeline (Pruitt et al., 2012).

The total size of the genome is 5,000,479 bp and has a GC content of 68.85%, larger than NCPPB 4393. A total of 4315 coding DNA sequences (CDSs) were predicted (Table 1). Of these, 2851 could be assigned to a COG (Clusters of Orthologous Groups) number. The most abundant COG category was "Signal transduction mechanisms" (407 proteins) followed by "General function prediction only" (388 proteins), "Transcription" (265 proteins), "Amino acid transport and metabolism" (250 proteins), and "Cell wall/membrane/envelope biogenesis" (237 proteins). In addition, 93 RNAs including rRNA and tRNA were identified.

As we know, Gram-negative bacteria including many *Xanthomonas* pathogens can use type III secretion system (T3SS) as virulence factor to attack host plants (Kay and Bonas, 2009). However, after screening the R1 genome, we cannot find T3SS, which is widely existed in many other *Xanthomonas* species. Except T3SS, this strain also lacks T6SS, which was first thought to be the representative of pathogenic and non-pathogenic *Xanthomonas* species (Shrivastava and Mande, 2008). These result indicated that strain R1 does not has pathogenicity on plants.

It has long been recognized that genomic island (GI) contributes to the evolution of bacteria and is important in bacterial

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Table 1
Genome feature of *X. sacchari* R1.

Attribute	Value
Genome size (bp)	5,000,479
DNA coding (bp)	4,273,989
G + C content (%)	68.85
Chromosome	1
Plasmid	1
Total genes	4408
Protein coding genes	4315
rRNA (5S, 16S, 23S)	2
tRNA	59
Genes with function prediction	3210
Genes assigned to COGs	2851

pathogenicity (Dobrindt et al., 2004). In this case, IslandViewer, which integrated several methods was used to predict the GI in R1 (Langille and Brinkman, 2009). Strikingly, we only got 28 CDS which are predicted to be GIs. This number is far fewer than the previously reports (Thieme et al., 2005; Jin et al., 2012). Interestingly, these 25 genes include 9 flagellar biosynthesis associated genes indicating their horizontal gene transfer origin, which has long been discussed in other bacteria (Lory et al., 2009). It has been well understood that flagellar systems contribute important role in biofilm formation in *Xanthomonas* species (Malamud et al., 2011). Since biofilm plays pivotal role in antagonism against other microorganism, we may infer that GIs, which were come from horizontal gene transfer, play some role in antagonistic ability in R1 strain.

Nucleotide sequence accession numbers

The complete chromosome sequence and two plasmid sequences have been deposited in GenBank under the accession number CP010409–CP010410. This strain has been deposited in CGMCC collection under the accession number of CGMCC 1.15149.

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